

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method

<130> 2601WOOP

<150> JP 10-374454

<151> 1998-12-28

<150> JP 11-122688

<151> 1999-04-28

<150> JP 11-249300

<151> 1999-09-02

<160> 24

<210> 1

<211> 16

<212> PRT

<213> Rat

*Sub
a'* <223> The 7th cystein residue binds with the 16th cystein residue to form
a intra-molecular disulfide-bond.

<400> 1

Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys

1

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<210> 2

<211> 19

<212> PRT

<213> Rat

<223> The 7th cystein residue binds with the 16th cystein residue to form
a intra-molecular disulfide-bond.

<400> 2

2/15

Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys

1

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Trp Gln Val

19

<210> 3

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 3

GTCGACATGG ATCTGCAAAC CTCGTTGCTG TG 32

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 4

ACTAGTTCAG GTGCCTTTGC TTTCTGTCCT CT 32

<210> 5

<211> 353

<212> PRT

<213> Rat

<400> 5

Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn

1

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See
at
end

3/15

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 20 25 30
 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
 35 40 45
 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
 50 55 60
 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
 65 70 75 80
 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
 85 90 95
 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
 100 105 110
 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
 115 120 125
 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
 130 135 140
 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
 145 150 155 160
 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
 165 170 175
 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
 180 185 190
 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
 195 200 205
 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
 210 215 220
 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala

Sub
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 cont

4/15

225 230 235 240
 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
 245 250 255
 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
 260 265 270
 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
 275 280 285
 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
 290 295 300
 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
 305 310 315 320
 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
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Thr

<210> 6

<211> 1074

<212> DNA

<213> Rat

<400> 6

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 ATCAACATCA TTATGCCTTC CGTGTTTGGT ACCATCTGTC TCCTGGGCAT CGTGGGAAAC 180
 TCCACGGTCA TCTTTGCTGT GGTGAAGAAG TCCAAGCTAC ACTGGTGCAG CAACGTCCCC 240
 GACATCTTCA TCATCAACCT CTCTGTGGTG GATCTGCTCT TCCTGCTGGG CATGCCTTTC 300
 ATGATCCACC AGCTCATGGG GAACGGCGTC TGGCACTTGG GGGAAACCAT GTGCACCCTC 360

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ATCACAGCCA TGGACGCCAA CAGTCAGTTC ACTAGCACCT ACATCCTGAC TGCCATGACC 420
 ATTGACCGCT ACTTGGCCAC CGTCCACCCC ATCTCCTCCA CCAAGTCCG GAAGCCCTCC 480
 ATGGCCACCC TGGTGATCTG CCTCCTGTGG GCGCTCTCCT TCATCAGTAT CACCCCTGTG 540
 TGGCTCTACG CCAGGCTCAT TCCCTTCCCA GGGGGTGCTG TGGGCTGTGG CATCCGCCTG 600
 CCAAACCCGG ACACTGACCT CTACTGGTTC ACTCTGTACC AGTTTTTCCT GGCCTTTGCC 660
 CTTCCGTTTG TGGTCATTAC CGCCGCATAC GTGAAAATAC TACAGCGCAT GACGTCTTCG 720
 GTGGCCCCAG CCTCCCAACG CAGCATCCGG CTTCGGACAA AGAGGGTGAC CCGCACGGCC 780
 ATTGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT GCAGCTGACC 840
 CAGCTGTCCA TCAGCCGCCG GACCCTCAGG TTTGTCTACT TGTACAACGC GGCCATCAGC 900
 TTGGGCTATG CTAACAGCTG CCTGAACCCC TTTGTGTACA TAGTGCTCTG TGAGACCTTT 960
 CGAAAACGCT TGGTGTTGTC AGTGAAGCCT GCAGCCCAGG GGCAGCTCCG CACGGTCAGC 1020
 AACGCTCAGA CAGCTGATGA GGAGAGGACA GAAAGCAAAG GCACCTGAAC TAGT 1074

<210> 7

<211> 326

<212> RNA

<213> Rat

<400> 7

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 AUCAGCUGUC UGAGCGUUGC UGACCGUGCG GAGCUCCCCC UGGGCUGCAG GCUUCACUGA 180
 CAACACCAAG CGUUUUCGAA AGGUCUCACA GAGCACUAUG UACACAAAGG GGUUCAGGCA 240
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<210> 8

<211> 18

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<213> Artificial Sequence

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6/15

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Sub
a1
cont

7/15

TCTTCCACGA AGTTCGGAA GCCCTCTGTG GCCACCCTGG TGATCTGCCT CCTGTGGGCC 720
 CTCTCCTTCA TCAGCATCAC CCCTGTGTGG CTGTATGCCA GACTCATCCC CTTCCCAGGA 780
 GGTGCAGTGG GCTGCGGCAT ACGCCTGCCC AACCCAGACA CTGACCTCTA CTGGTTCACC 840
 CTGTACCAGT TTTTCCTGGC CTTTGCCCTG CCTTTTGTGG TCATCACAGC CGCATACGTG 900
 AGGATCCTGC AGCGCATGAC GTCCTCAGTG GCCCCGCGCT CCCAGCGCAG CATCCGGCTG 960
 CGGACAAAGA GGGTGACCCG CACAGCCATC GCCATCTGTC TGGTCTTCTT TGTGTGCTGG 1020
 GCACCCTACT ATGTGCTACA GCTGACCCAG TTGTCCATCA GCCGCCCGAC CCTCACCTTT 1080
 GTCTACTTAT ACAATGCGGC CATCAGCTTG GGCTATGCCA ACAGCTGCCT CAACCCCTTT 1140
 GTGTACATCG TGCTCTGTGA GACGTTCCGC AAACGCTTGG TCCTGTGGT GAAGCCTGCA 1200
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<210> 11

<211> 422

<212> PRT

<213> Human

<400> 11

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Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 50 55 60

Thr Gly Thr Gly Trp MeT Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

Sub
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8/15

85 90 95
 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile MeT
 100 105 110
 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
 115 120 125
 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
 130 135 140
 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
 145 150 155 160
 Phe Leu Leu Gly MeT Pro Phe MeT Ile His Gln Leu MeT Gly Asn Gly
 165 170 175
 Val Trp His Phe Gly Glu Thr MeT Cys Thr Leu Ile Thr Ala MeT Asp
 180 185 190
 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala MeT Ala Ile
 195 200 205
 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
 210 215 220
 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
 225 230 235 240
 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
 245 250 255
 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
 260 265 270
 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
 275 280 285
 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg MeT
 290 295 300

See
 at
 cont

9/15

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
 305 310 315 320
 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
 325 330 335
 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
 340 345 350
 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
 355 360 365
 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
 370 375 380
 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
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<210> 12

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 12

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<210> 13

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<212> DNA

See
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10/15

<213> Artificial Sequence

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<223>

<400> 13

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<210> 14

<211> 33

<212> DNA

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<210> 15

<211> 33

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<220>

<223>

<400> 15

AACTAGTTCA GGTGCCTTTG CTTTCTGTCC TCT 33

<210> 16

<211> 1074

<212> DNA

<213> Human

<400> 16

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See
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cont

11/15

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 TCCACGGTCA TCTTCGCGGT CGTGAAGAAG TCCAAGCTGC ACTGGTGCAA CAACGTCCCC 240
 GACATCTTCA TCATCAACCT CTCGGTAGTA GATCTCCTCT TTCTCCTGGG CATGCCCTTC 300
 ATGATCCACC AGCTCATGGG CAATGGGGTG TGGCACTTTG GGGAGACCAT GTGCACCCTC 360
 ATCACGGCCA TGGATGCCAA TAGTCAGTTC ACCAGCACCT ACATCCTGAC CGCCATGGCC 420
 ATTGACCGCT ACCTGCCAC TGTCCACCCC ATCTCTTCCA CGAAGTTCCG GAAGCCCTCT 480
 GTGGCCACCC TGGTGATCTG CCTCCTGTGG GCCCTCTCCT TCATCAGCAT CACCCCTGTG 540
 TGGCTGTATG CCAGACTCAT CCCCTTCCCA GGAGGTGCAG TGGGCTGCGG CATACGCCTG 600
 CCCAACCCAG AACTGACCT CTACTGGTTC ACCCTGTACC AGTTTTTCCT GGCCTTTGCC 660
 CTGCCTTTTG TGGTCATCAC AGCCGCATAC GTGAGGATCC TGCAGCGCAT GACGTCCTCA 720
 GTGGCCCCCG CCTCCCAGCG CAGCATCCGG CTGCGGACAA AGAGGGTGAC CCGCACAGCC 780
 ATCGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT ACAGCTGACC 840
 CAGTTGTCCA TCAGCCGCCC GACCCTCACC TTTGTCTACT TATACAATGC GGCCATCAGC 900
 TTGGGCTATG CCAACAGCTG CCTCAACCOC TTTGTGTACA TCGTGCTCTG TGAGACGTTT 960
 CGCAAACGCT TGGTCCTGTC GGTGAAGCCT GCAGCCCAGG GGCAGCTTCG CGCTGTCAGC 1020
 AACGCTCAGA CGGCTGACGA GGAGAGGACA GAAAGCAAAG GCACCTGAAC TAGT 1074

<210> 17

<211> 1283

<212> DNA

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<400> 17

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 GGGACAAGGT GGCAGGCGCT GGAGGCTGCC GCAGCCTGCG TGGGTGGAGG GGAGCTCAGC 180
 TCGGTTGTGG GAGCAGGCGA CCGGCACTGG CTGGATGGAC CTGGAAGCCT CGCTGCTGCC 240
 CACTGGTCCC AACGCCAGCA ACACCTCTGA TGGCCCCGAT AACCTCACTT CGGCAGGATC 300

See
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ACCTCCTCGC ACGGGGAGCA TCTCCTACAT CAACATCATC ATGCCTTCGG TGTTCGGCAC 360
 CATCTGCCCTC CTGGGCATCA TCGGGAATC CACGGTCATC TTCGCGGTCG TGAAGAAGTC 420
 CAAGCTGCAO TGGTGCAACA ACGTCCCCGA CATCTTCATC ATCAACCTCT CGGTAGTAGA 480
 TCTCCTCTTT CTCCTGGGCA TGCCCTTCAT GATCCACCAG CTCATGGGCA ATGGGGTGTG 540
 GCACTTTGGG GAGACCATGT GCACCCTCAT CACGGCCATG GATGCCAATA GTCAGITCAC 600
 CAGCACCTAC ATCTGACCG CCATGGCCAT TGACCGCTAC CTGGCCACTG TCCACCCCAT 660
 CTCTTCCACG AAGTTCGGA AGCCCTCTGT GGCCACCCTG GTGATCTGCC TCCTGTGGGC 720
 CCTCTCCTTC ATCAGCATCA CCCCTGTGTG GCTGTATGCC AGACTCATCC CCTTCCCAGG 780
 AGGTGCAGTG GGCTGCGCA TACGCCTGCC CAACCCAGAC ACTGACCTCT ACTGGTTCAC 840
 CCTGTACCAG TTTTTCCTGG CCTTTGCCCT GCCTTTTGTG GTCATCACAG CCGCATACGT 900
 GAGGATCCTG CAGCGCATGA CGTCCTCAGT GGCCCCGCC TCCCAGCGCA GCATCCGGCT 960
 GCGGACAAAG AGGGTGACCC GCACAGCCAT CGCCATCTGT CTGGTCTTCT TTGTGTGCTG 1020
 GGCACCCTAC TATGTGCTAC AGCTGACCCA GTTGTCCATC AGCCGCCCGA CCCTCACCTT 1080
 TGTCTACTTA TACAATGCGG CCATCAGCTT GGGCTATGCC AACAGCTGCC TCAACCCCTT 1140
 TGTGTACATC GTGCTCTGTG AGACGTTCGG CAAACGCTTG GTCCTGTCGG TGAAGCCTGC 1200
 AGCCCAGGGG CAGCTTCGCG CTGTCAGCAA CGCTCAGACG GCTGACGAGG AGAGGACAGA 1260
 AAGCAAAGGC ACCTGAACTA GTT 1283

<210> 18

<211> 420

<212> RNA

<213> Human

<400> 18

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 GCUGCAGGCU UCACCGACAG GACCAAGCGU UUGCGGAACG UCUCACAGAG CACGAUGUAC 180
 ACAAAGGGGU UGAGGCAGCU GUUGGCAUAG CCAAGCUGA UGGCCGCAU GUUAAGUAG 240
 ACAAAGGUGA GGGUCGGGCG GCUGAUGGAC AACUGGGUCA GCUGUAGCAC AUAGUAGGGU 300

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13/15

GCCCAGCACA CAAAGAAGAC CAGACAGAUG GCGAUGGCUG UGCGGGUCAC CCUCUUUGUC 360

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<210> 19

<211> 18

<212> PRT

<213> Rat

<223> The 6th cystein residue binds with the 15th cystein residue to form
a intra-molecular disulfide-bond.

<400> 19

Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp

1 5 10 15

Gln Val

18

<210> 20

<211> 17

<212> PRT

<213> Rat

<223> The 5th cystein residue binds with the 14th cystein residue to form
a intra-molecular disulfide-bond.

<400> 20

Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln

1 5 10 15

Val

17

<210> 21

<211> 16

<212> PRT

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14/15

<213> Rat

<223> The 4th cystein residue binds with the 13th cystein residue to form
a intra-molecular disulfide-bond.

<400> 21

Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val

1

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15 16

<210> 22

<211> 15

<212> PRT

<213> Rat

<223> The 3rd cystein residue binds with the 12th cystein residue to form
a intra-molecular disulfide-bond.

<400> 22

Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val

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10

15

<210> 23

<211> 14

<212> PRT

<213> Rat

<223> The 2nd cystein residue binds with the 11th cystein residue to form
a intra-molecular disulfide-bond.

<400> 23

Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val

1

5

10

<210> 24

<211> 13

<212> PRT

See
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cont

15/15

<213> Rat

<223> The 1st cystein residue binds with the 10th cystein residue to form
a intra-molecular disulfide-bond.

<400> 24

Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val

1

5

10

See
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cont